Pre-Q1 riboswitch, *B. subtilis* **ENERGY = -11.8**

Green: **Pair in both structures**
Red: **Pair in Accepted Structure only**
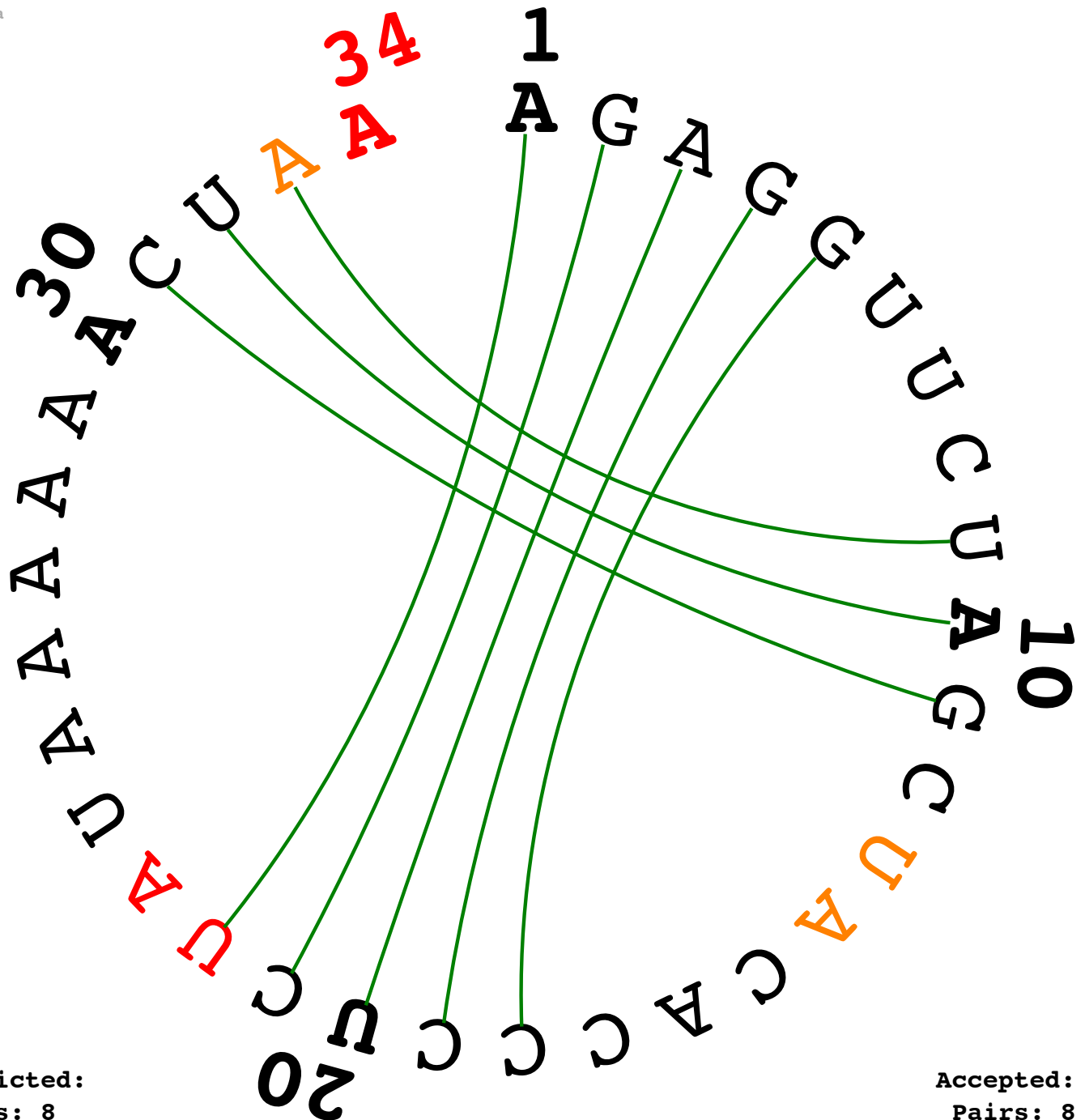**Purple: Pair in Predicted Structure only**

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 8 / 8 = 100.00%
PPV: 8 / 8 = 100.00%

Predicted:
Pairs: 8
Pseudoknotted Pairs: 3

Accepted:
Pairs: 8
Pseudoknotted Pairs: 3

Telomerase pseudoknot, human ENERGY = -37.2

Green: Pair in both structures
Red: Pair in Accepted Structure only
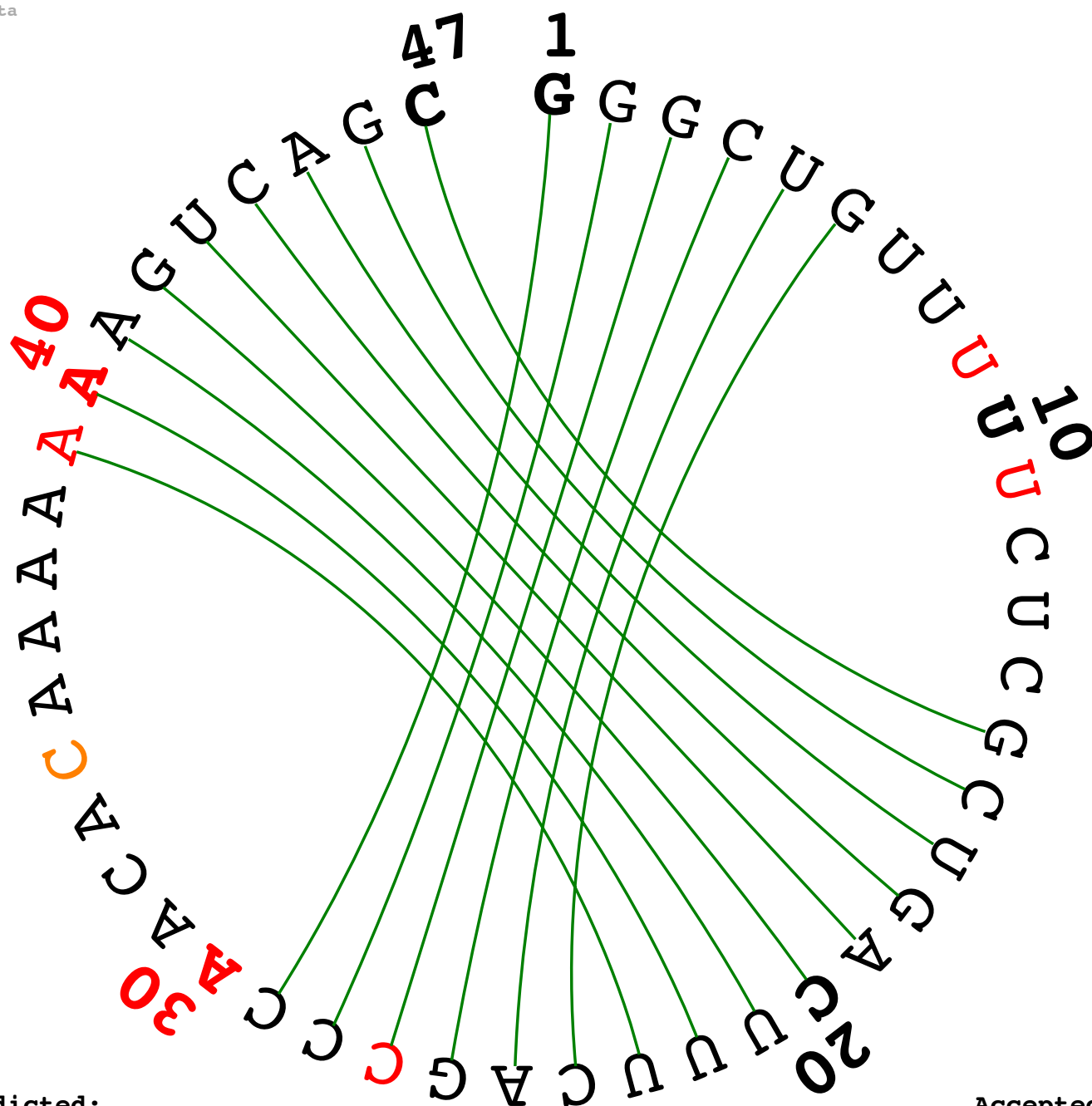Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 15 / 15 = 100.00%
PPV: 15 / 15 = 100.00%

Predicted:
Pairs: 15
Pseudoknotted Pairs: 6

Accepted:
Pairs: 15
Pseudoknotted Pairs: 6

tRNA(asp), yeast ENERGY = -46.9

Green: Pair in both structures
Red: Pair in Accepted Structure only
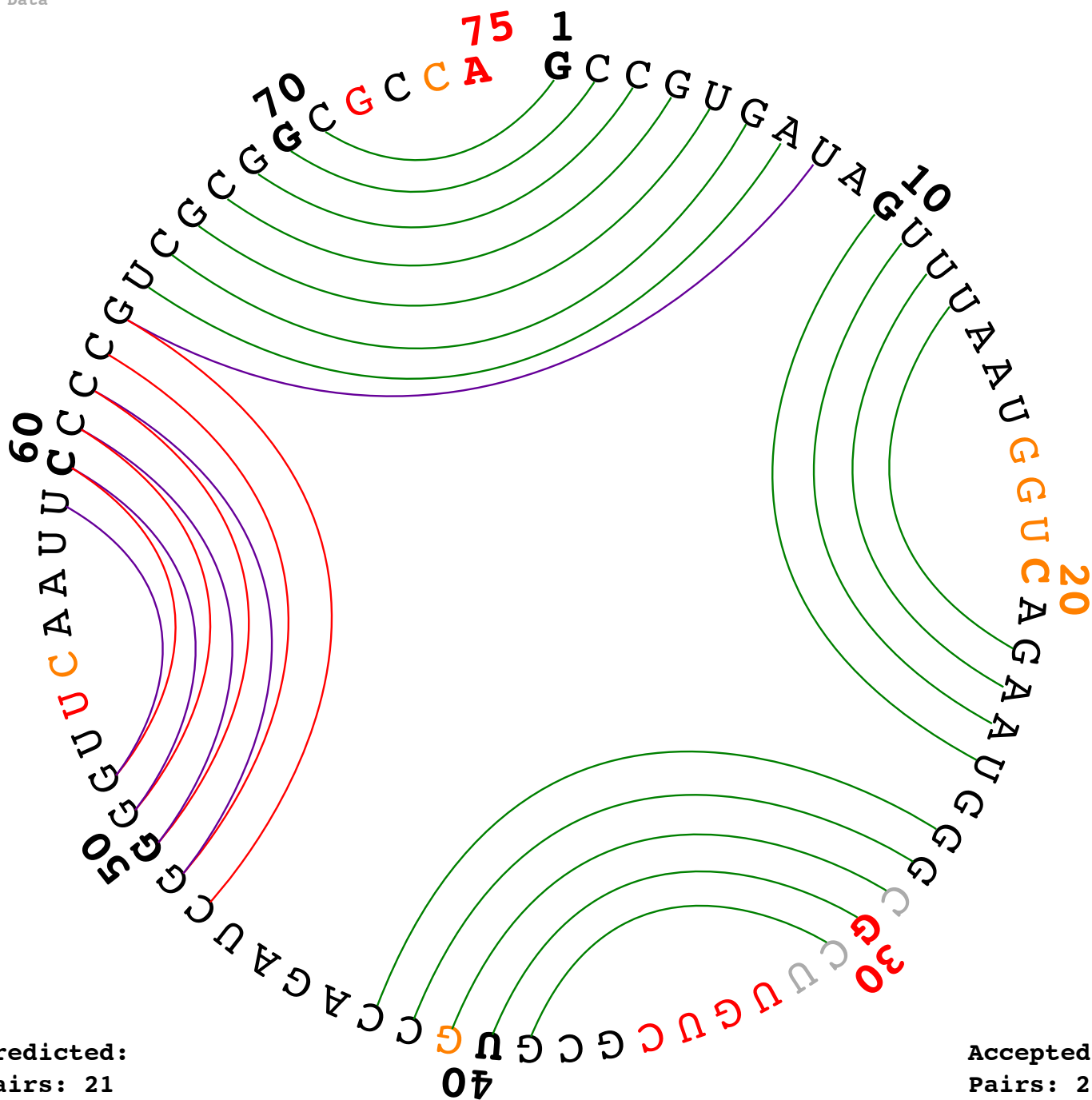Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 20 / 21 = 95.24%
PPV: 20 / 21 = 95.24%
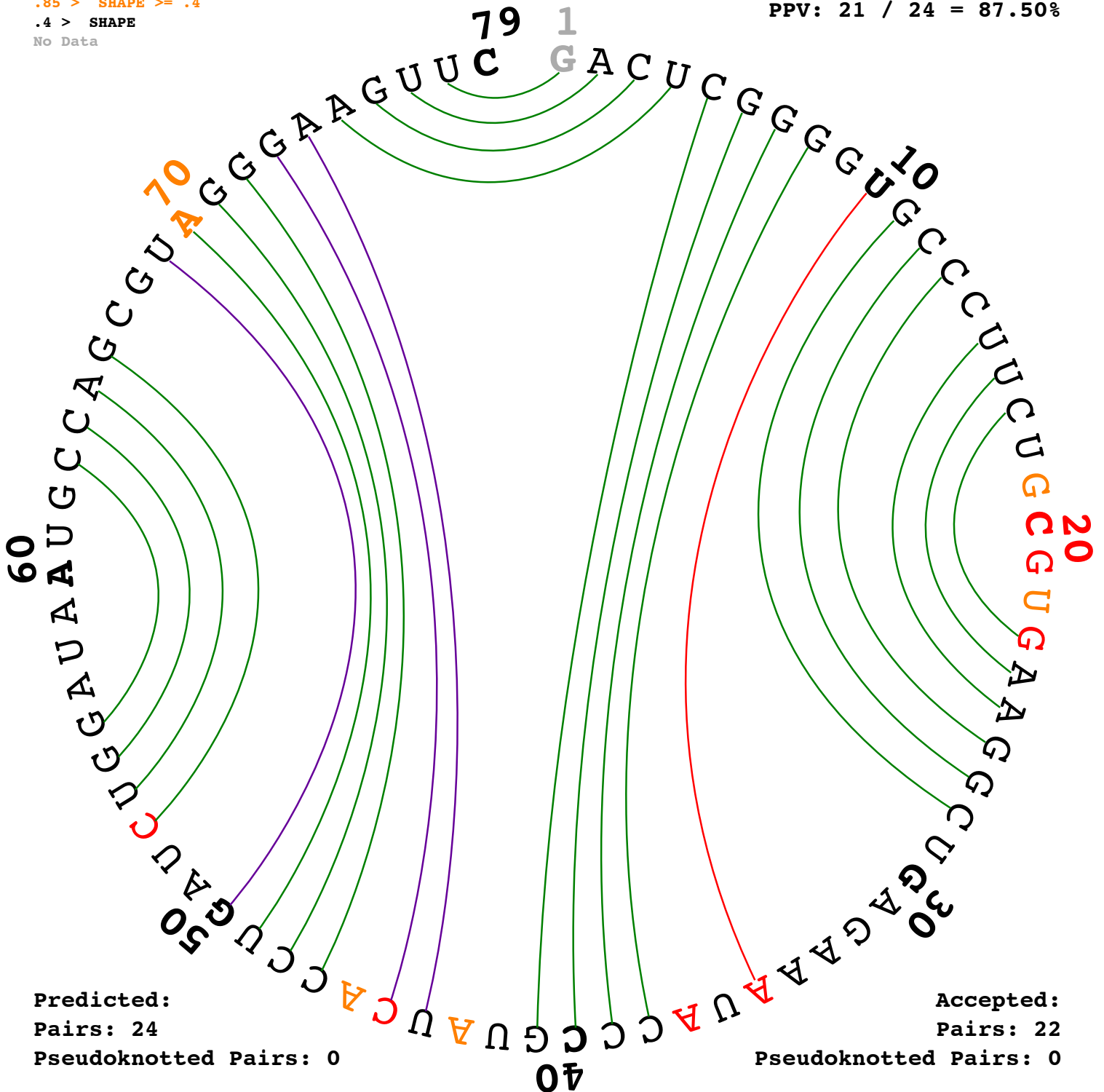
Predicted:
Pairs: 21
Pseudoknotted Pairs: 0

Accepted:
Pairs: 21
Pseudoknotted Pairs: 0

TPP riboswitch, *E. coli* ENERGY = −45.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 21 / 22 = 95.45%
PPV: 21 / 24 = 87.50%

Predicted:
Pairs: 24
Pseudoknotted Pairs: 0

Accepted:
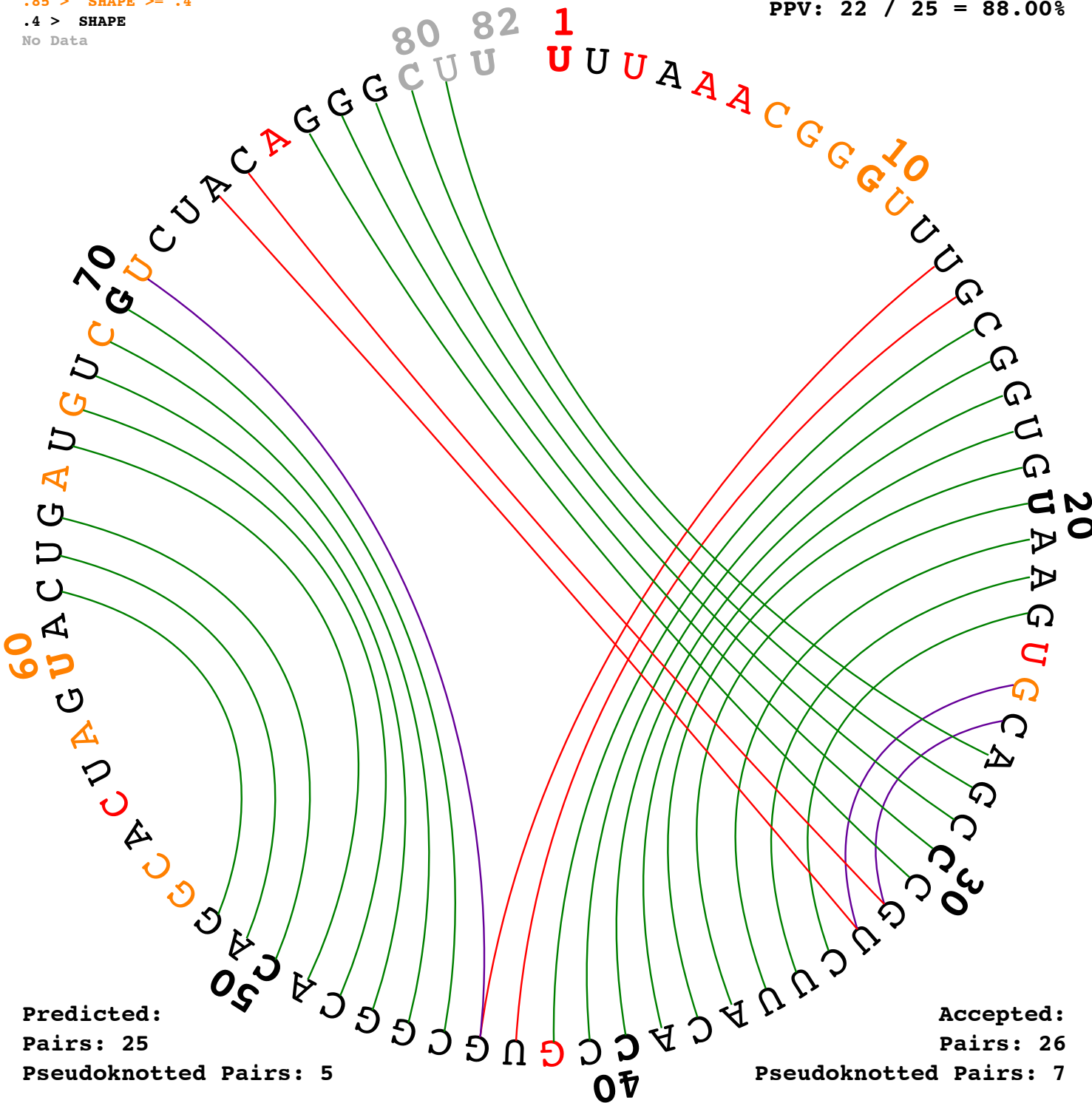Pairs: 22
Pseudoknotted Pairs: 0

SARS corona virus pseudoknot ENERGY = -55.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 22 / 26 = 84.62%
PPV: 22 / 25 = 88.00%

Predicted:
Pairs: 25
Pseudoknotted Pairs: 5

Accepted:
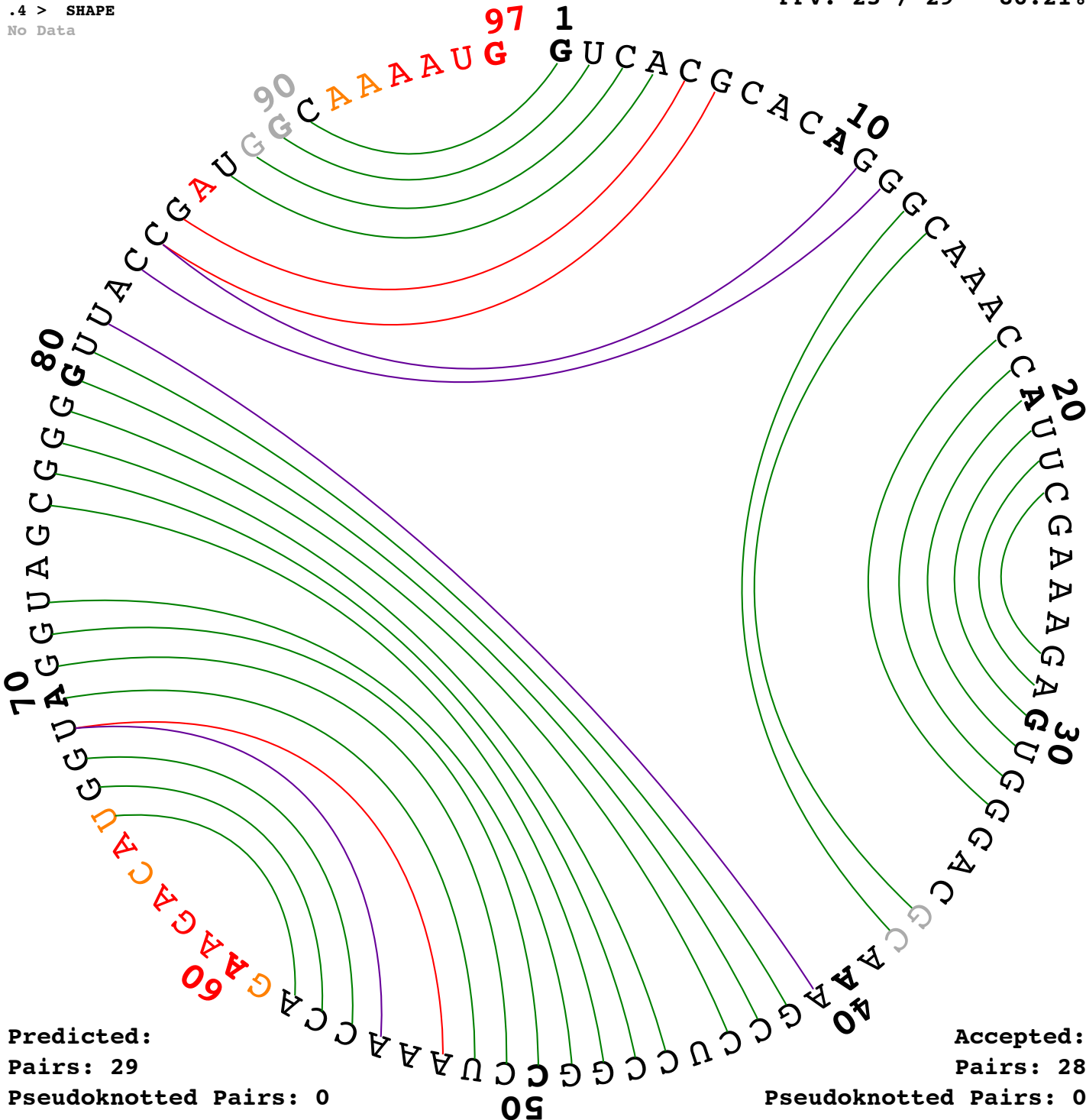Pairs: 26
Pseudoknotted Pairs: 7

cyclic-di-GMP riboswitch, *V. cholerae*   ENERGY = -66.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

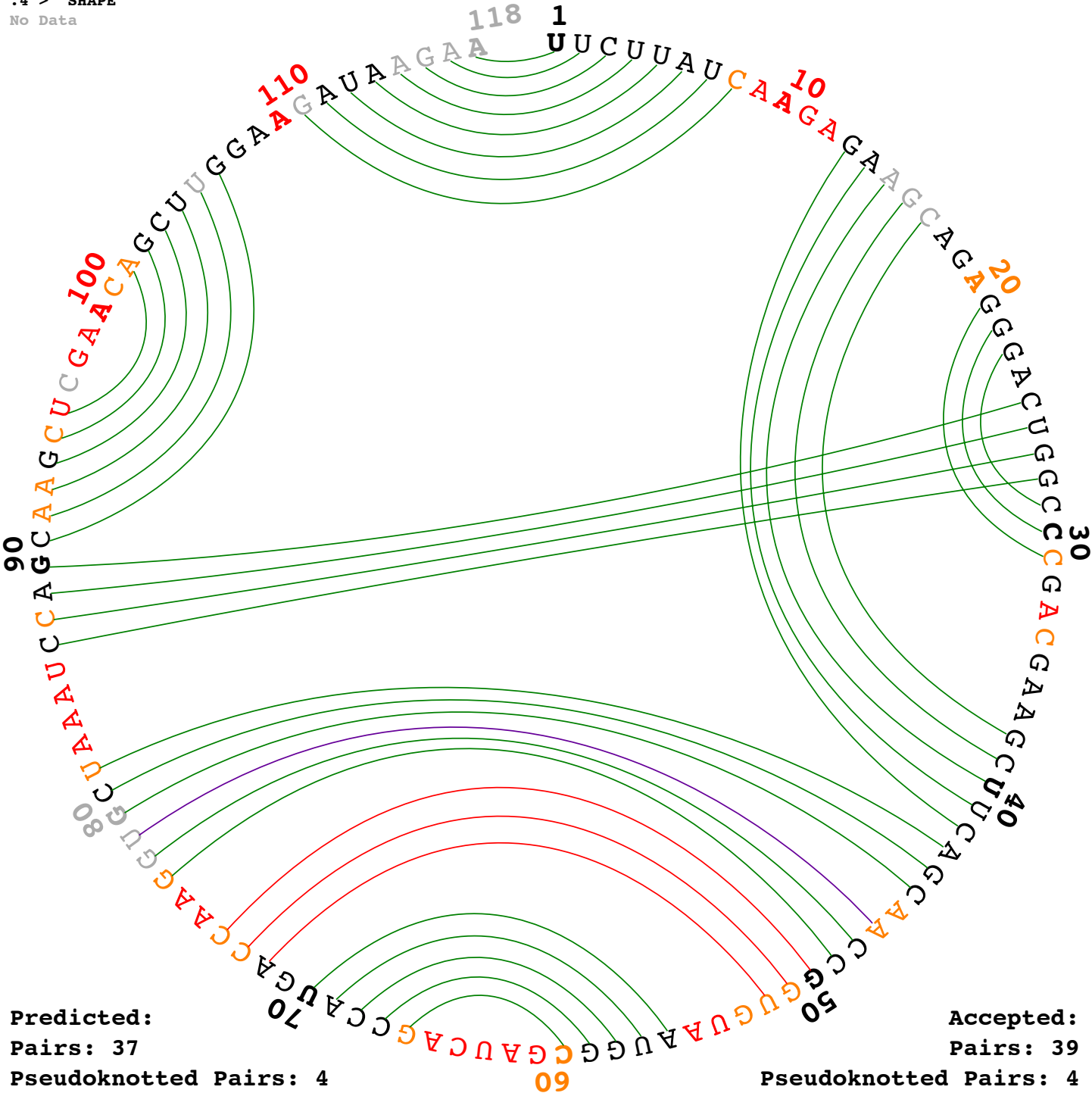Sensitivity: 25 / 28 = 89.29%
PPV: 25 / 29 = 86.21%

Predicted:
Pairs: 29
Pseudoknotted Pairs: 0

Accepted:
Pairs: 28
Pseudoknotted Pairs: 0

SAM I riboswitch, *T. tengcongensis* **ENERGY = -65.6**

Green: **Pair in both structures**
Red: **Pair in Accepted Structure only**
Purple: **Pair in Predicted Structure only**

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 36 / 39 = 92.31%
PPV: 36 / 37 = 97.30%

Predicted:
Pairs: 37
Pseudoknotted Pairs: 4

Accepted:
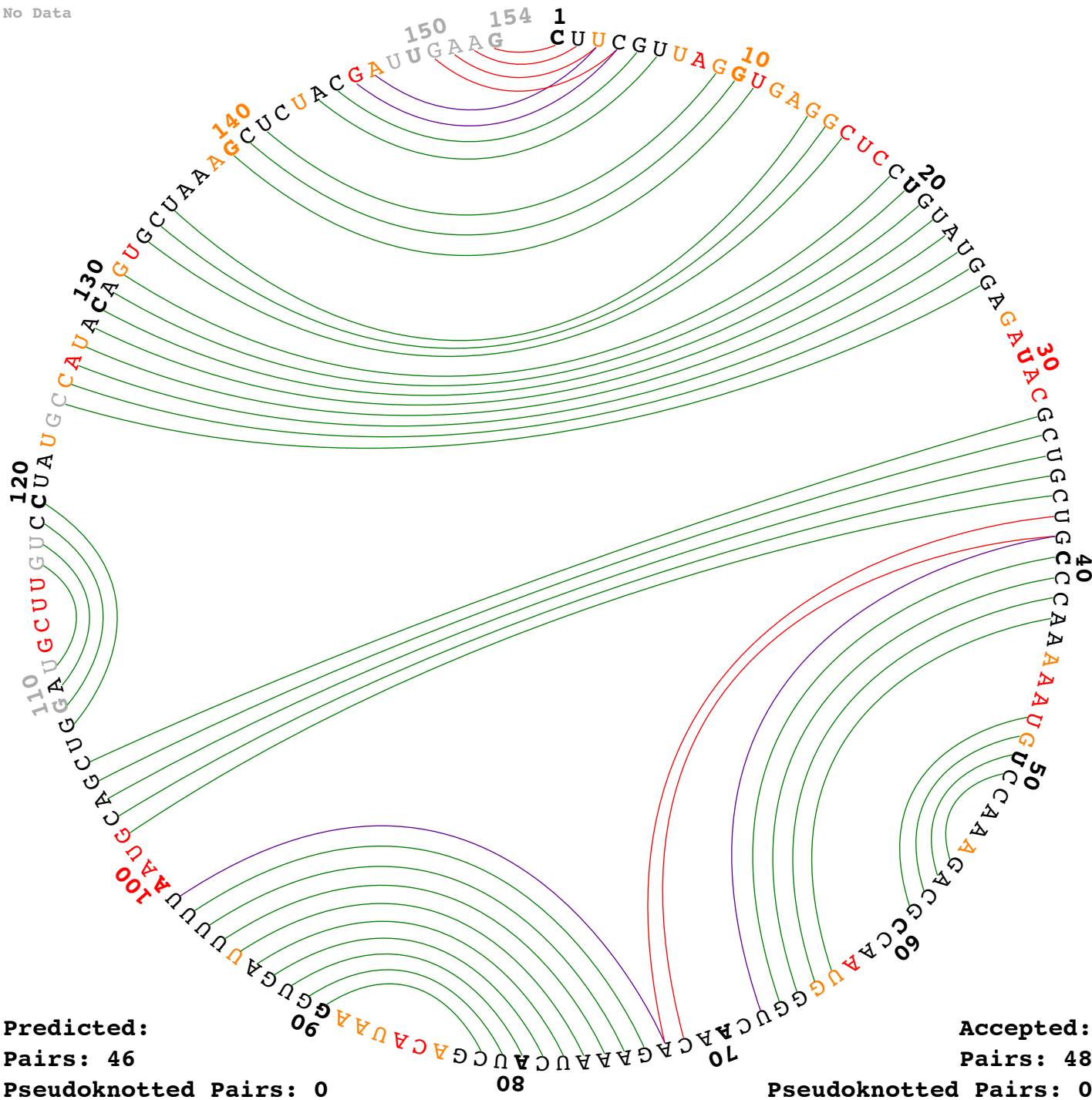Pairs: 39
Pseudoknotted Pairs: 4

M-Box riboswitch, *B. subtilis* ENERGY = -80.5

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 42 / 48 = 87.50%
PPV: 42 / 46 = 91.30%

Predicted:
Pairs: 46
Pseudoknotted Pairs: 0

Accepted:
Pairs: 48
Pseudoknotted Pairs: 0

P546 domain, bI3 group I intron ENERGY = -81.0

Green: Pair in both structures
Red: Pair in Accepted Structure only
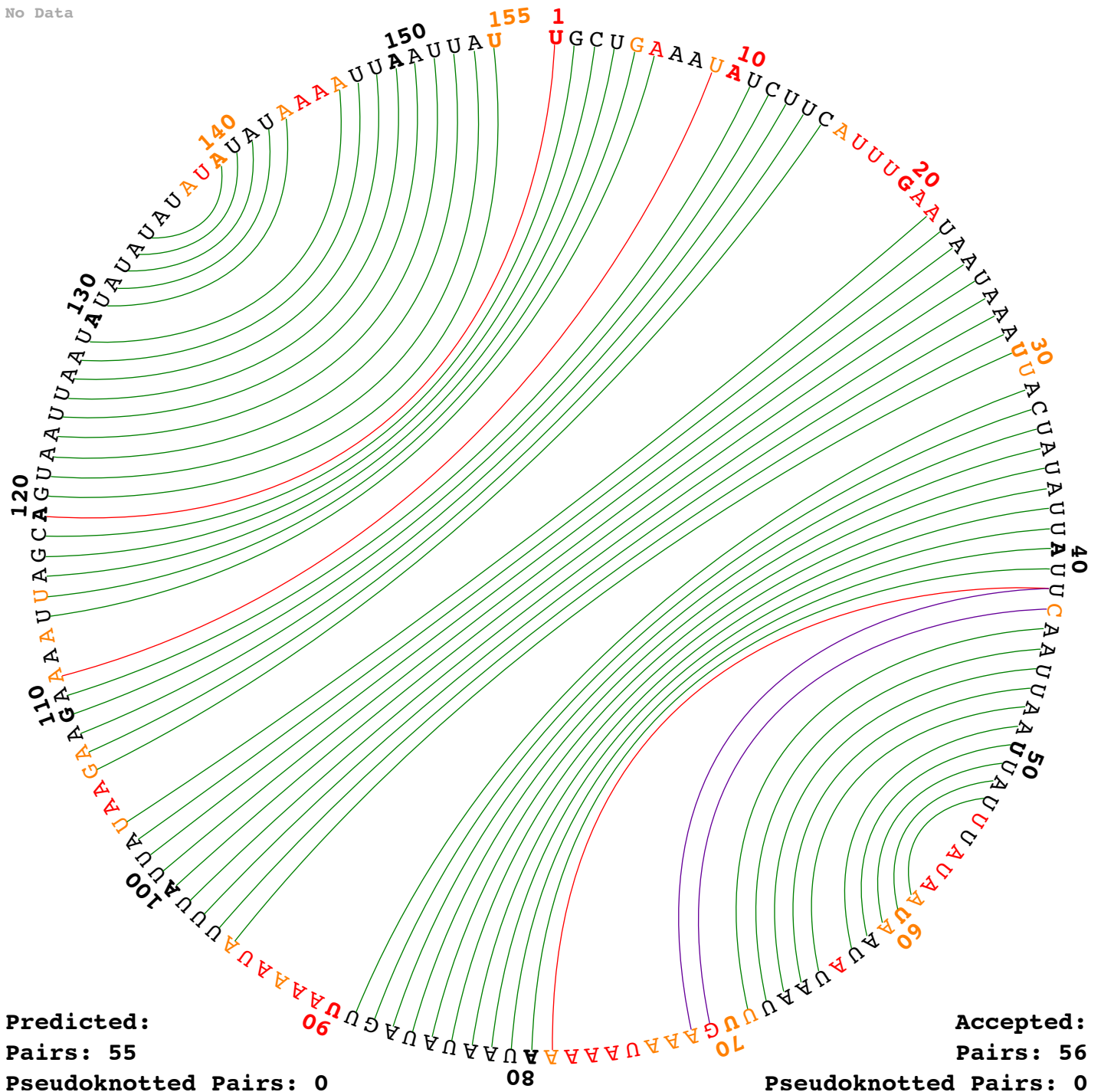Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 53 / 56 = 94.64%
PPV: 53 / 55 = 96.36%

Predicted:
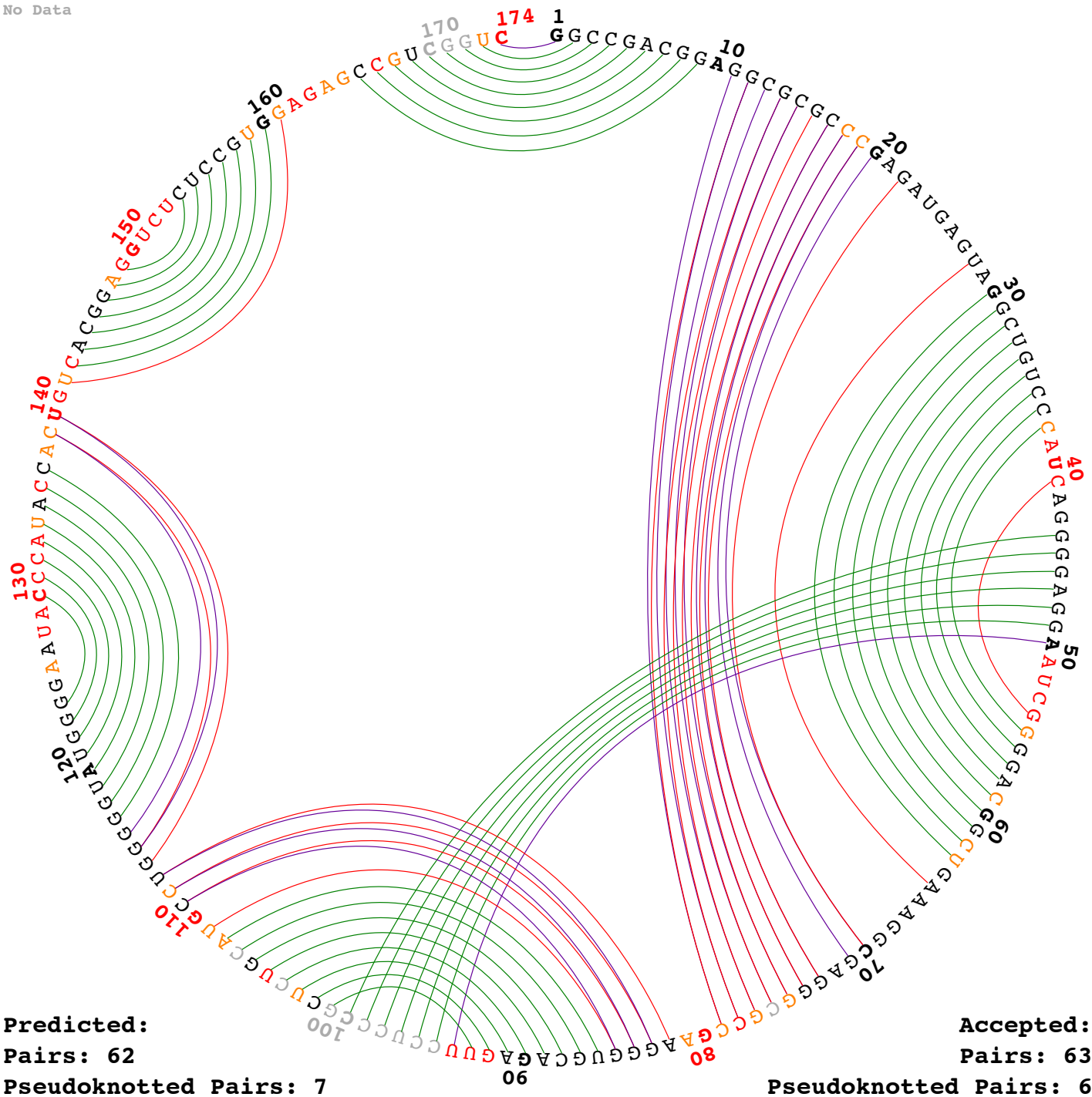Pairs: 55
Pseudoknotted Pairs: 0

Accepted:
Pairs: 56
Pseudoknotted Pairs: 0

Lysine riboswitch, *T. maritima* **ENERGY = –119.8**

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

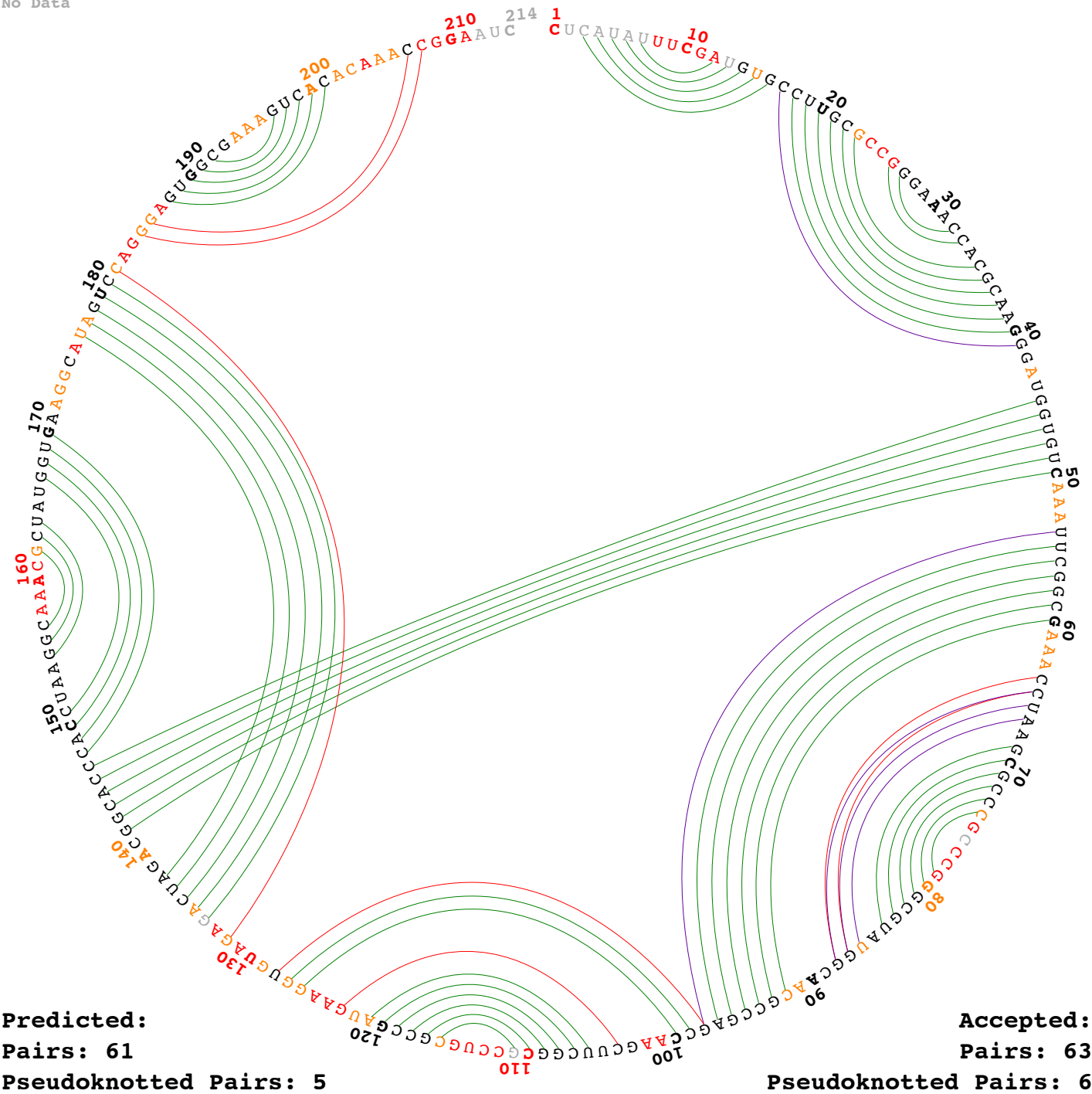Sensitivity: 55 / 63 = 87.30%
PPV: 55 / 62 = 88.71%

Predicted:
Pairs: 62
Pseudoknotted Pairs: 7

Accepted:
Pairs: 63
Pseudoknotted Pairs: 6

Group I intron, *Azoarcus sp.* **ENERGY = –123.3**

Green: **Pair in both structures**
Red: **Pair in Accepted Structure only**
Purple: **Pair in Predicted Structure only**

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 58 / 63 = 92.06%
PPV: 58 / 61 = 95.08%

Predicted:
Pairs: 61
Pseudoknotted Pairs: 5

Accepted:
Pairs: 63
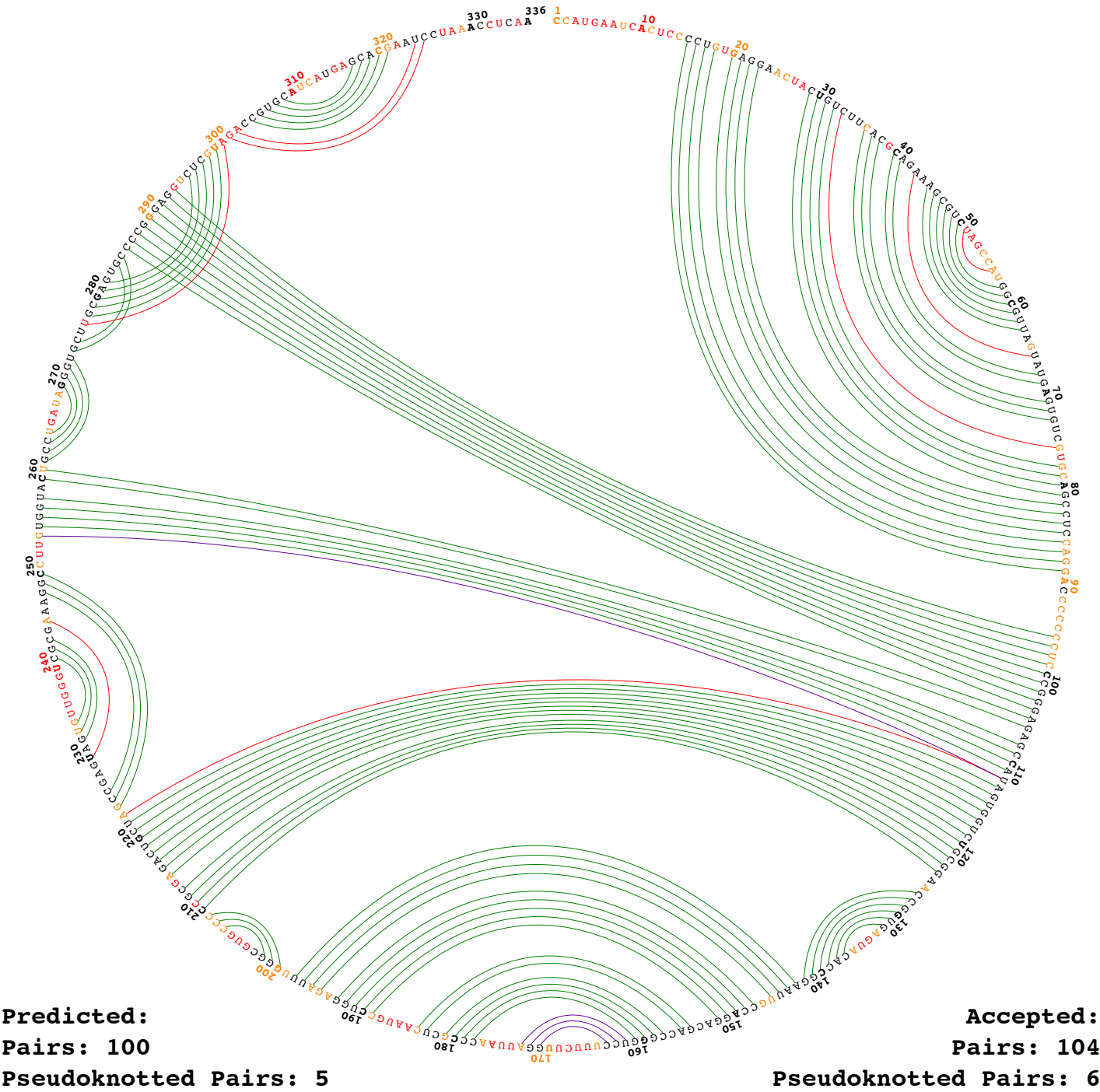**Pseudoknotted Pairs: 6**

Hepatitis C virus IRES domain ENERGY = –190.7

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

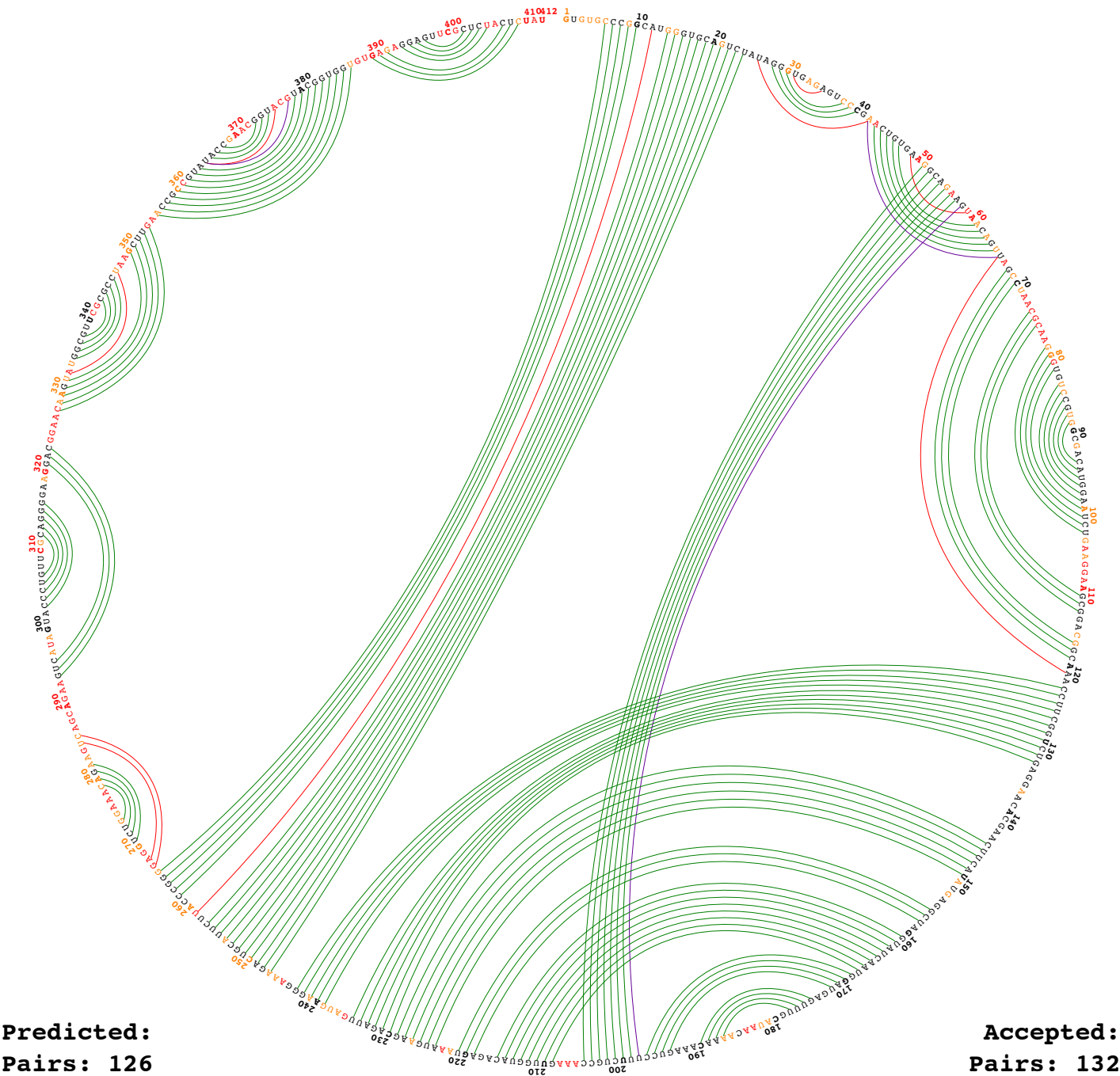Sensitivity: 96 / 104 = 92.31%
PPV: 96 / 100 = 96.00%

Predicted:
Pairs: 100
Pseudoknotted Pairs: 5

Accepted:
Pairs: 104
Pseudoknotted Pairs: 6

Group II intron, *O. iheyensis* ENERGY = −240.4

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 123 / 132 = 93.18%
PPV: 123 / 126 = 97.62%

Predicted:
Pairs: 126
Pseudoknotted Pairs: 8
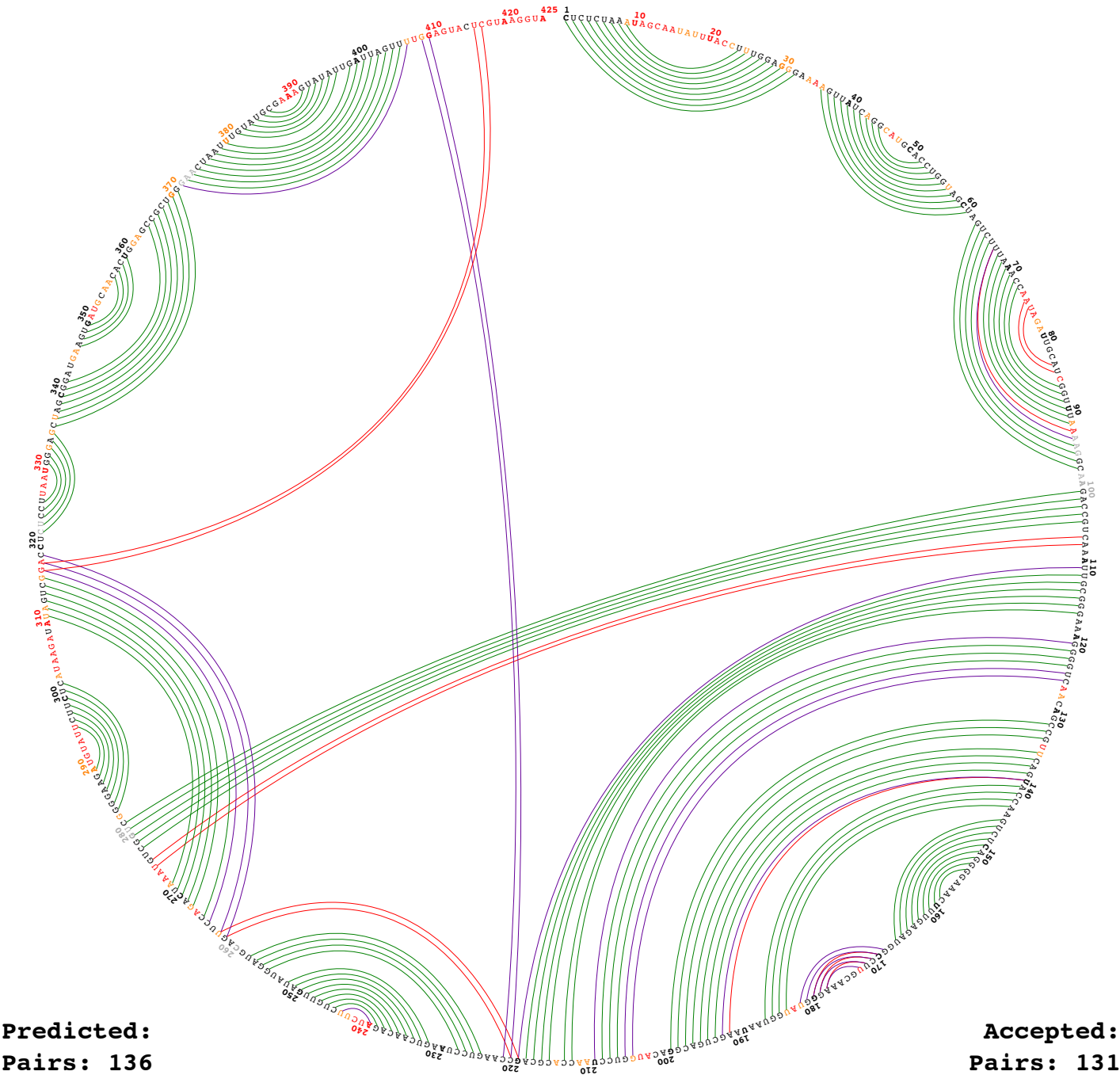
Accepted:
Pairs: 132
Pseudoknotted Pairs: 7

Group I Intron, *T. thermophila* ENERGY = –302.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 123 / 131 = 93.89%
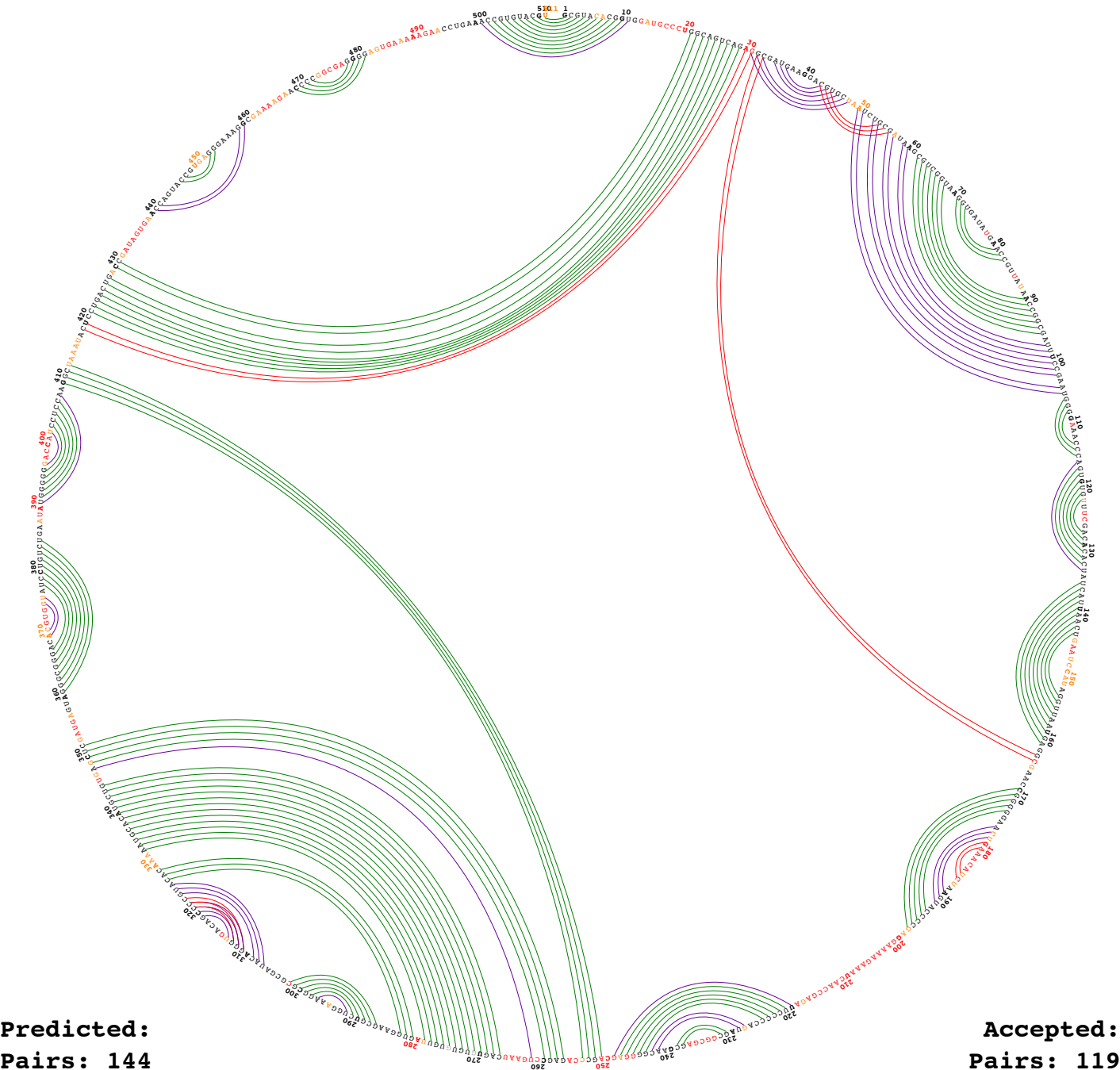PPV: 124 / 136 = 91.18%

Predicted:
Pairs: 136
Pseudoknotted Pairs: 5

Accepted:
Pairs: 131
Pseudoknotted Pairs: 6

5' domain of 23S rRNA, *E. coli* **ENERGY = −328.2**

Green: **Pair in both structures**
Red: **Pair in Accepted Structure only**
Purple: **Pair in Predicted Structure only**

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 110 / 119 = 92.44%
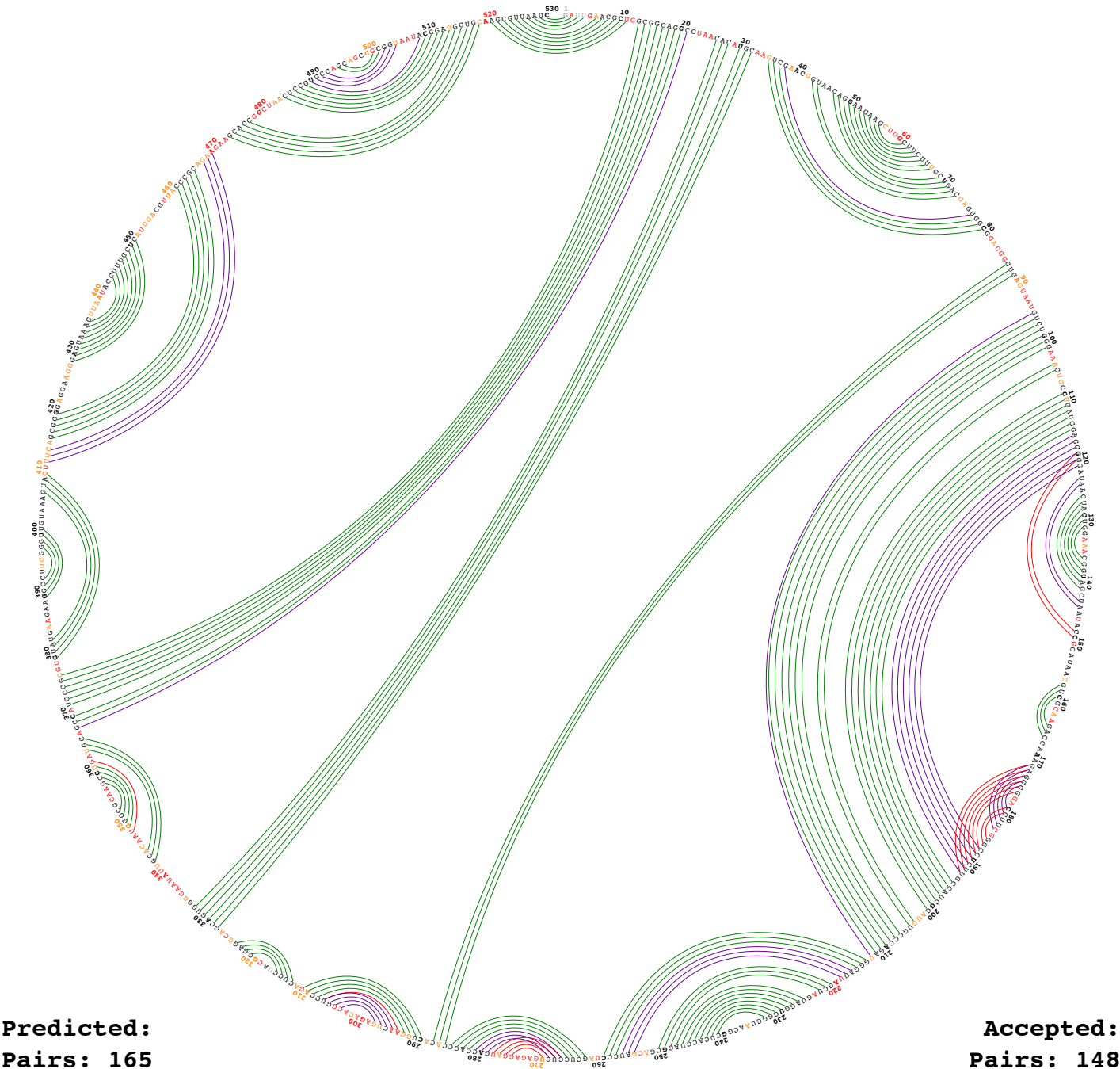**PPV: 110 / 144 = 76.39%**

Predicted:
Pairs: 144
Pseudoknotted Pairs: 0

Accepted:
Pairs: 119
Pseudoknotted Pairs: 0

5' domain of 16S rRNA, _E. coli_ ENERGY = –371.0

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 133 / 148 = 89.86%
PPV: 133 / 165 = 80.61%

Predicted:
Pairs: 165
Pseudoknotted Pairs: 0

Accepted:
Pairs: 148
Pseudoknotted Pairs: 0

Fluoride riboswitch, *P. syringae* **ENERGY = -40.5**

Green: **Pair in both structures**
Red: **Pair in Accepted Structure only**
Purple: **Pair in Predicted Structure only**

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 15 / 16 = 93.75%
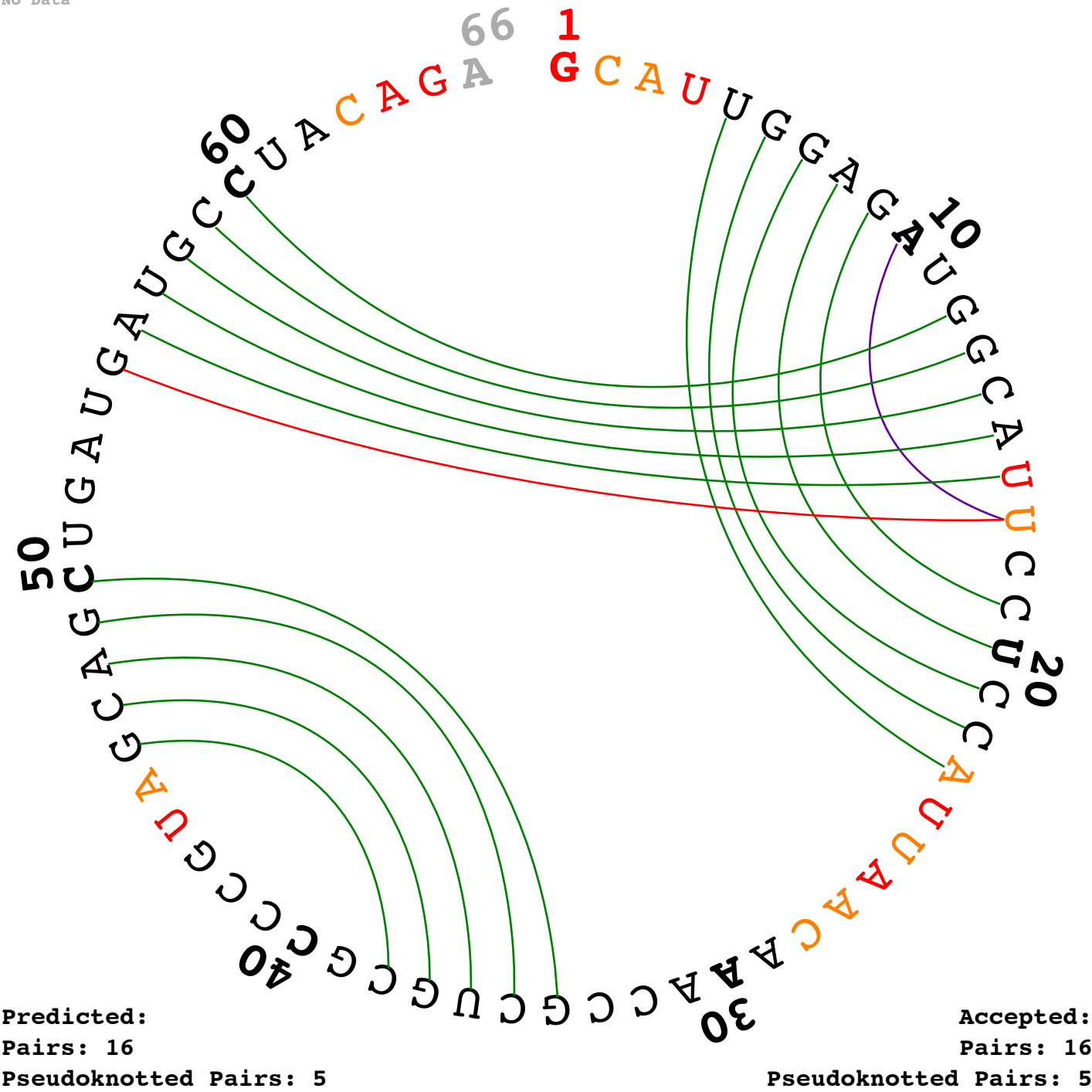PPV: 15 / 16 = 93.75%

Predicted:
Pairs: 16
Pseudoknotted Pairs: 5

Accepted:
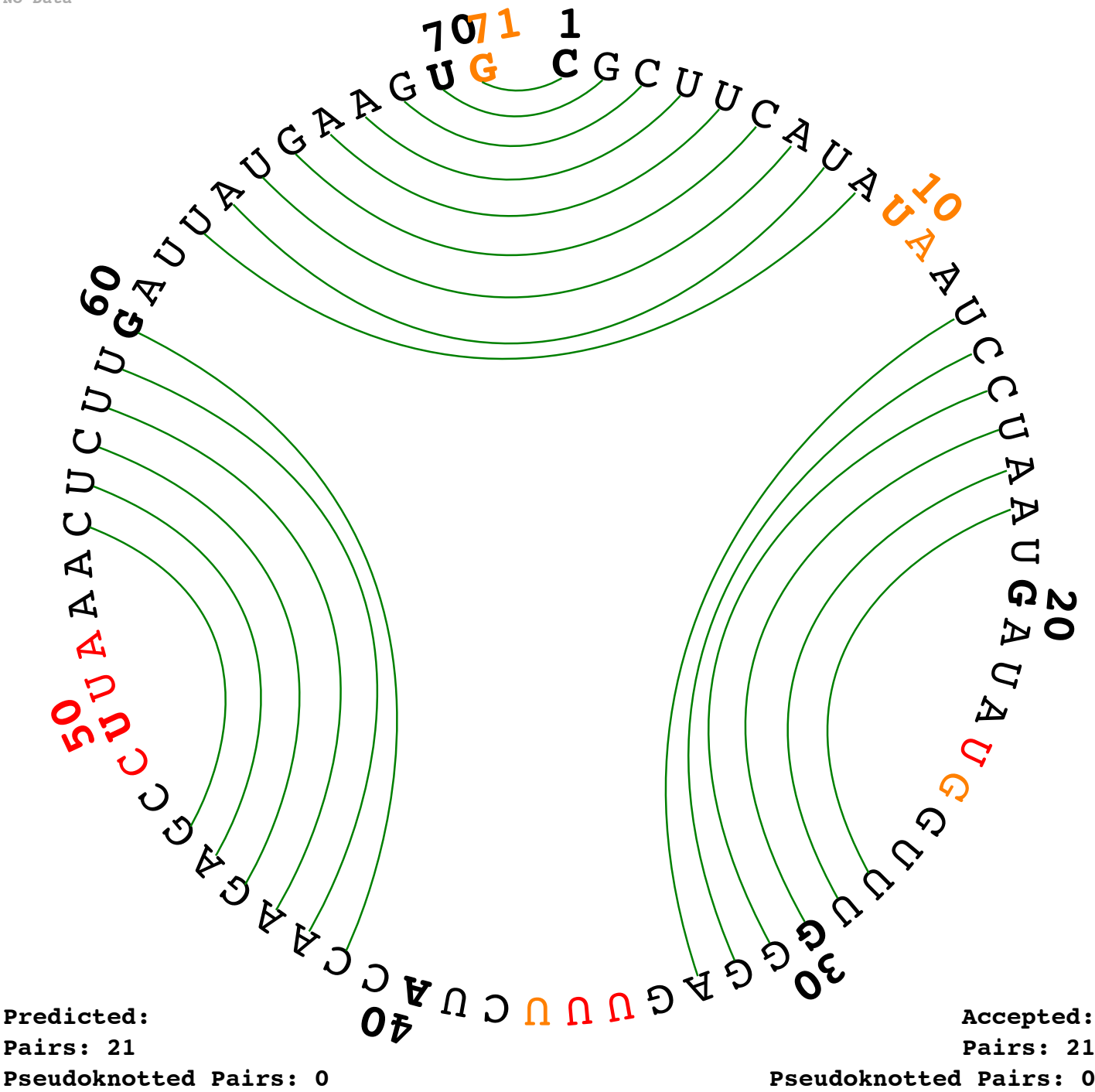Pairs: 16
Pseudoknotted Pairs: 5

Adenine riboswitch, *V. vulnificus* ENERGY = -47.8

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 21 / 21 = 100.00%
PPV: 21 / 21 = 100.00%

Predicted:
Pairs: 21
Pseudoknotted Pairs: 0

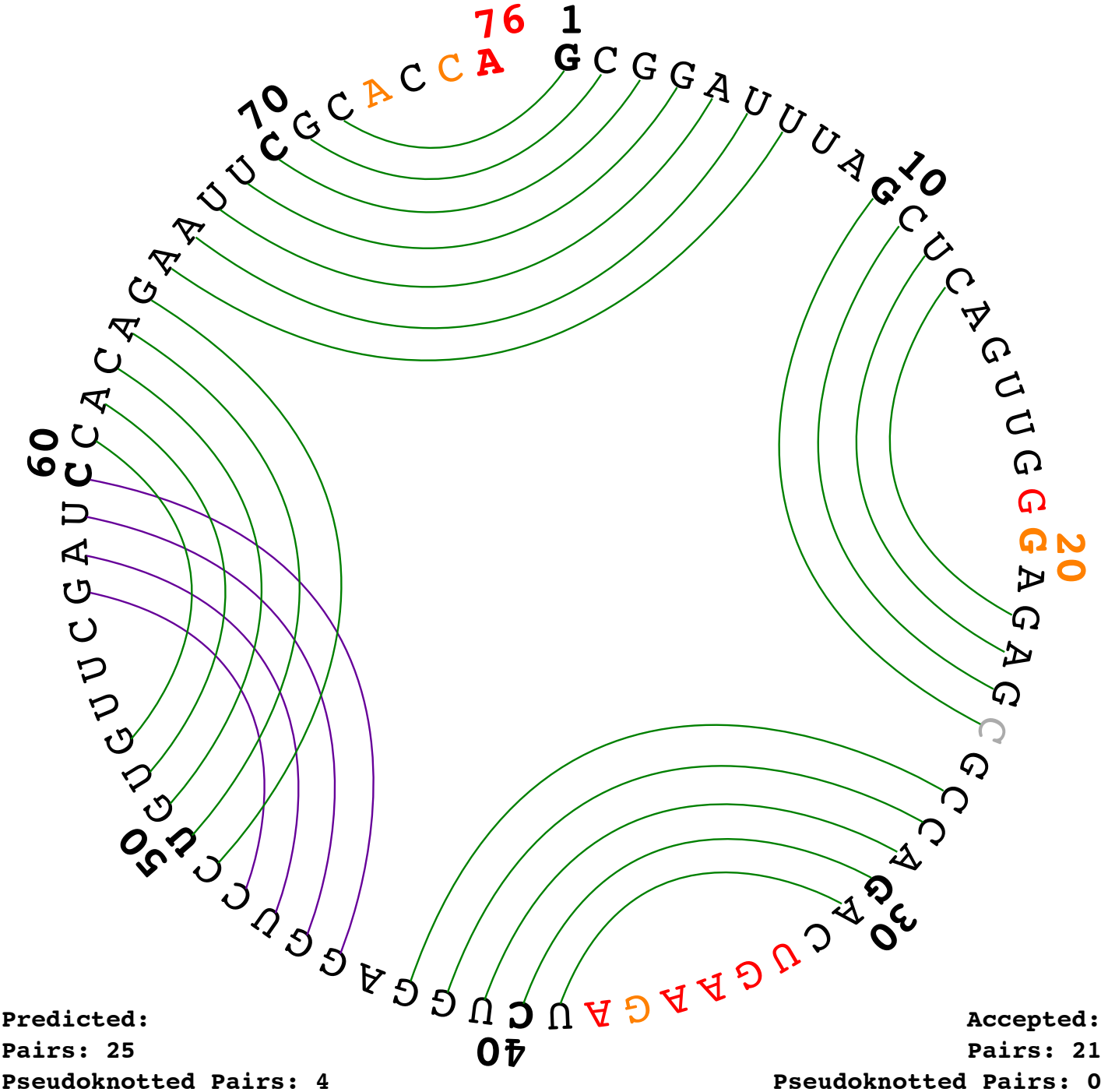Accepted:
Pairs: 21
Pseudoknotted Pairs: 0

tRNA(phe), *E. coli* ENERGY = -64.4

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 21 / 21 = 100.00%
PPV: 21 / 25 = 84.00%

Predicted:
Pairs: 25
Pseudoknotted Pairs: 4

Accepted:
Pairs: 21
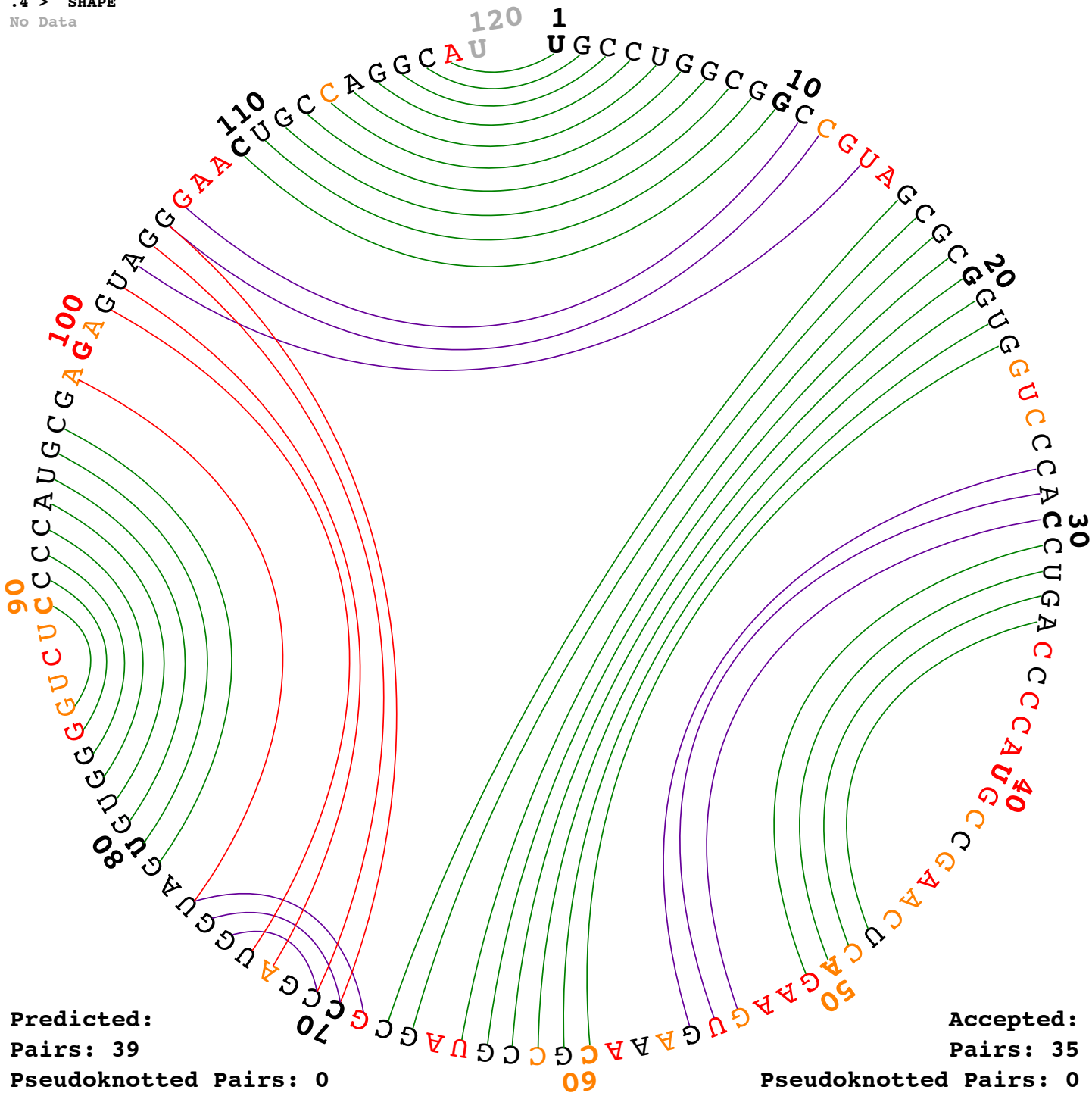Pseudoknotted Pairs: 0

5S rRNA, *E. coli* ENERGY = -76.7

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data
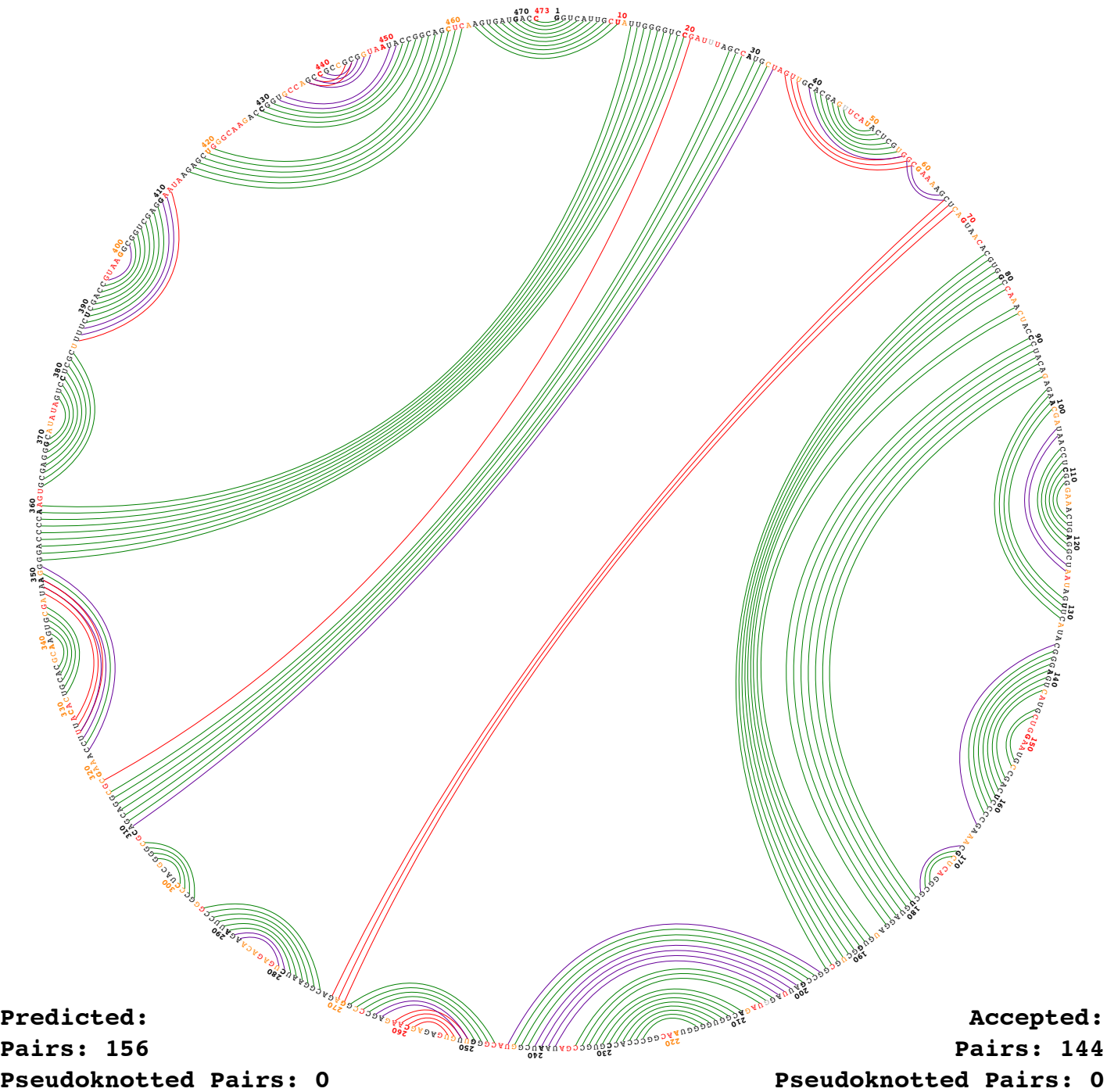
Sensitivity: 30 / 35 = 85.71%
PPV: 30 / 39 = 76.92%

Predicted:
Pairs: 39
Pseudoknotted Pairs: 0

Accepted:
Pairs: 35
Pseudoknotted Pairs: 0

5' domain of 16S rRNA, *H. volcanii* **ENERGY = −368.9**

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 129 / 144 = 89.58%
PPV: 129 / 156 = 82.69%

Predicted:
Pairs: 156
Pseudoknotted Pairs: 0

Accepted:
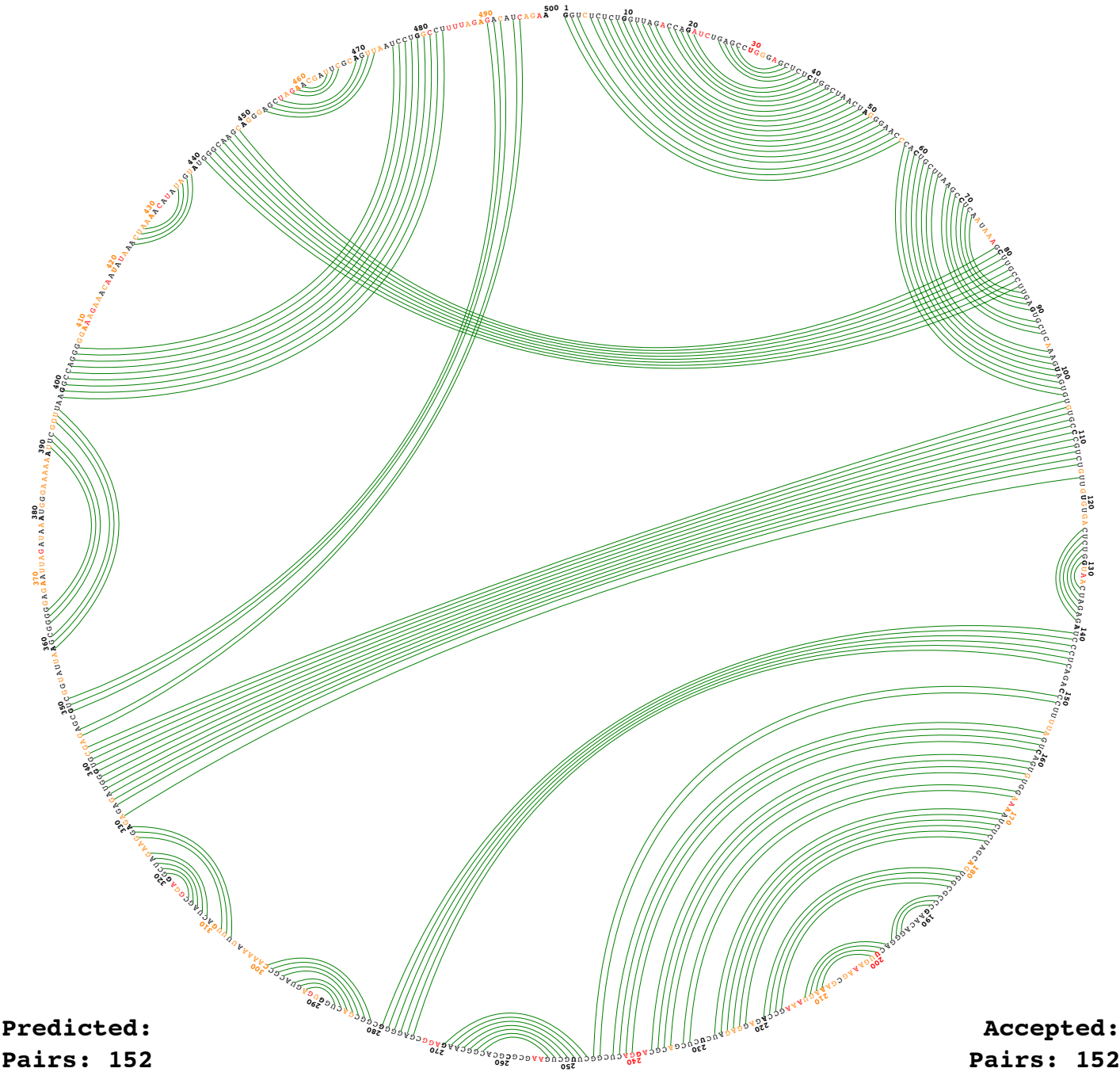**Pairs: 144**
Pseudoknotted Pairs: 0

HIV-1 5' pseudoknot domain ENERGY = -292.2

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 152 / 152 = 100.00%
PPV: 152 / 152 = 100.00%
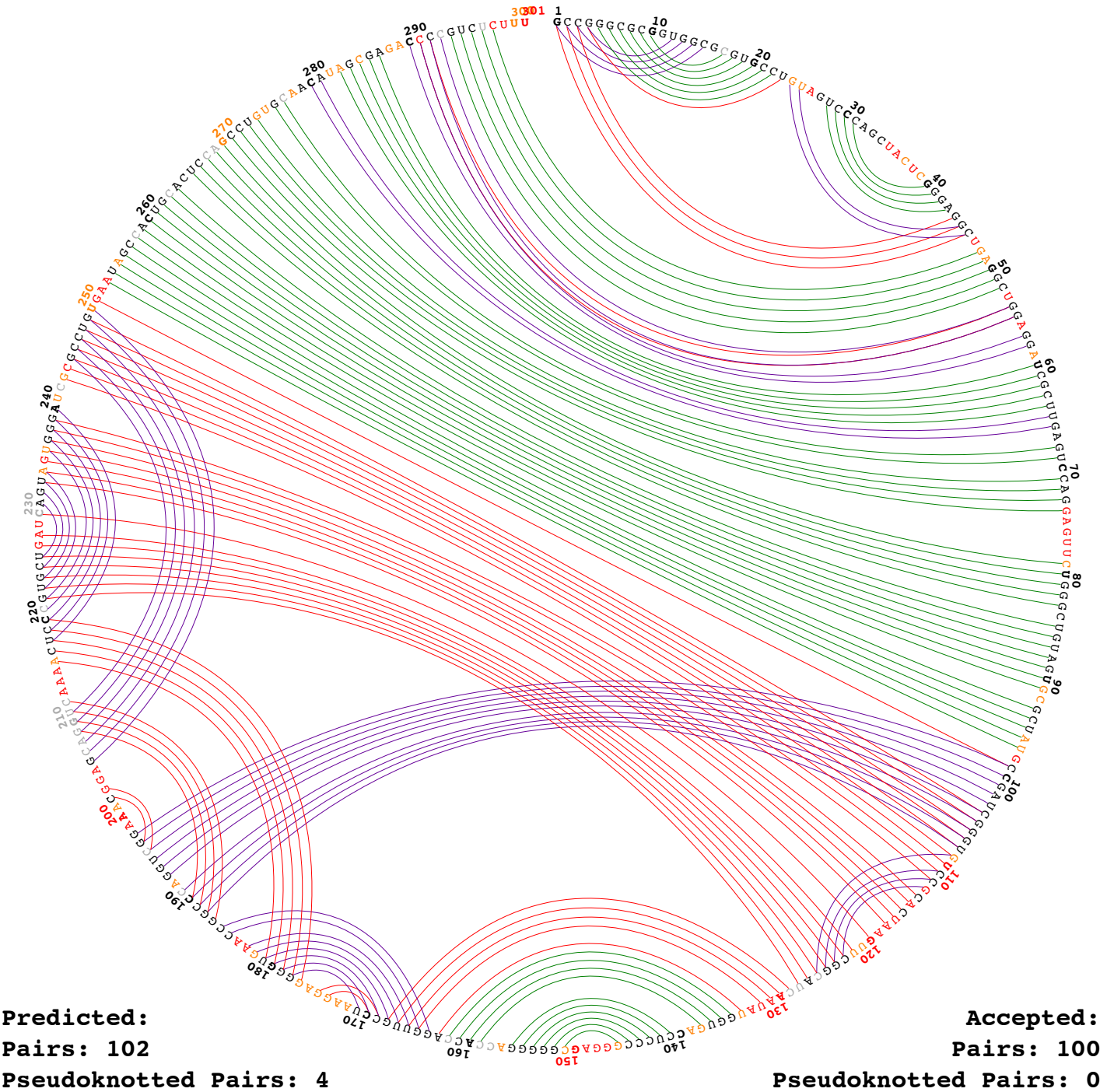
Predicted:
Pairs: 152
Pseudoknotted Pairs: 8

Accepted:
Pairs: 152
Pseudoknotted Pairs: 8

Signal recognition particle RNA, human ENERGY = -202.6

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

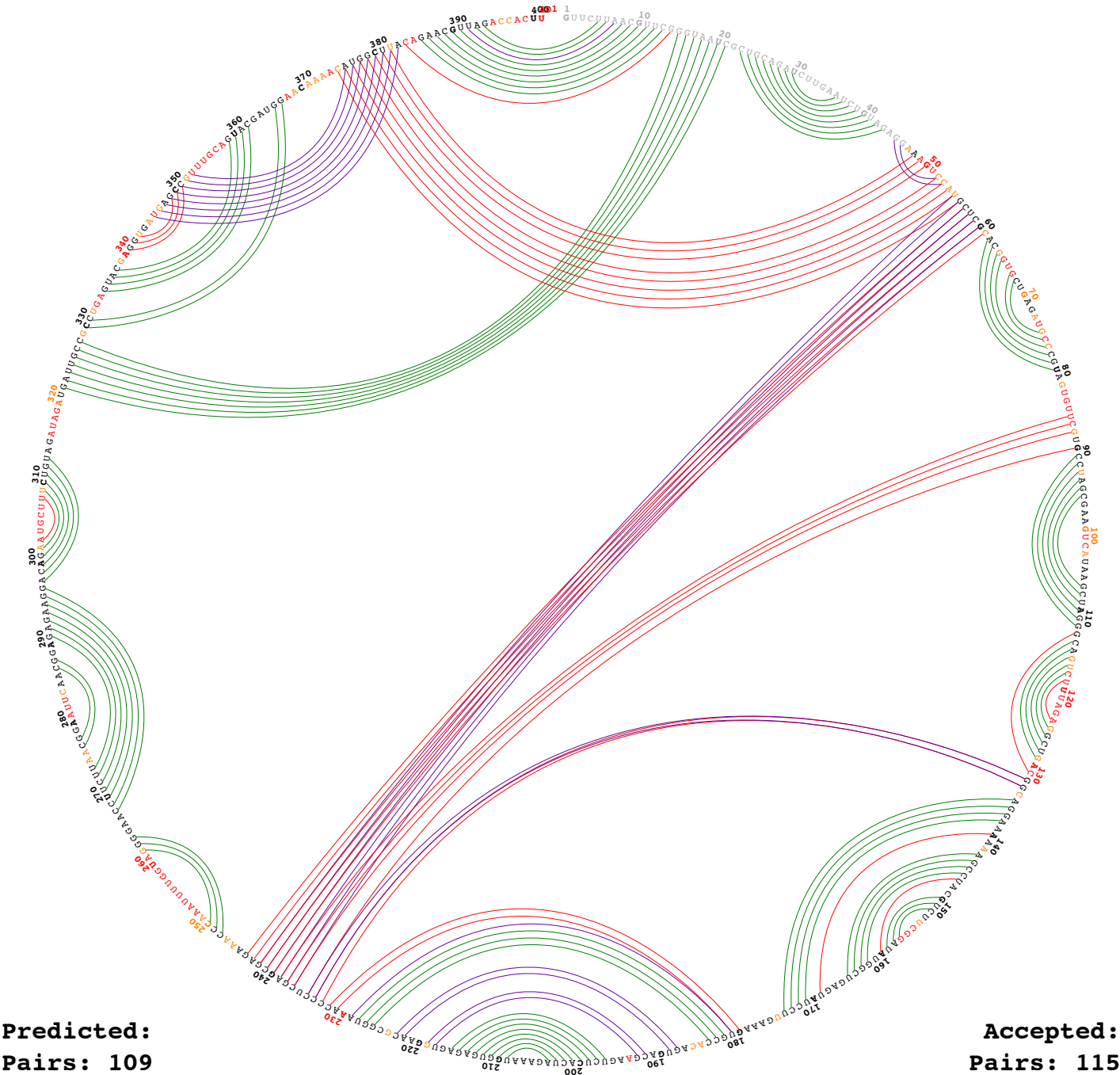Sensitivity: 55 / 100 = 55.00%
PPV: 55 / 102 = 53.92%

Predicted:
Pairs: 102
Pseudoknotted Pairs: 4

Accepted:
Pairs: 100
Pseudoknotted Pairs: 0

RNase P, *B. subtilis* ENERGY = −201.7

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 87 / 115 = 75.65%
PPV: 87 / 109 = 79.82%

Predicted:
Pairs: 109
Pseudoknotted Pairs: 6

Accepted:
Pairs: 115
Pseudoknotted Pairs: 7